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Entered 8/2/01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/617,099B

DATE: 08/02/2001

TIME: 16:59:16

Input Set : A:\P19771.ST25.txt

Output Set: N:\CRF3\08022001\I617099B.raw

ENTERED

3 <110> APPLICANT: Seino, Susumu
 4 Shibasaki, Tadao
 5 Ozaki, Nobuaki
 7 <120> TITLE OF INVENTION: Protein Rim2
 9 <130> FILE REFERENCE: P19771
 11 <140> CURRENT APPLICATION NUMBER: 09/617,099B
 12 <141> CURRENT FILING DATE: 2000-07-14
 14 <150> PRIOR APPLICATION NUMBER: JP 288372/99
 15 <151> PRIOR FILING DATE: 1999-10-08
 17 <160> NUMBER OF SEQ ID NOS: 5
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1590
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Mus musculus
 26 <400> SEQUENCE: 1
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 29 1 5 10 15
 31 Ala Ser Gln Pro Pro Pro Gln Pro Glu Met Pro Asp Leu Ser His Leu
 32 20 25 30
 34 Thr Glu Glu Glu Arg Lys Ile Ile Leu Ala Val Met Asp Arg Gln Lys
 35 35 40 45
 37 Lys Glu Glu Glu Lys Glu Gln Ser Val Leu Lys Ile Lys Glu Glu His
 38 50 55 60
 40 Lys Ala Gln Pro Thr Gln Trp Phe Pro Phe Ser Gly Ile Thr Glu Leu
 41 65 70 75 80
 43 Val Asn Asn Val Leu Gln Pro Gln Gln Lys Gln Pro Asn Glu Lys Glu
 44 85 90 95
 46 Pro Gln Thr Lys Leu His Gln Gln Phe Glu Met Tyr Lys Glu Gln Val
 47 100 105 110
 49 Lys Lys Met Gly Glu Glu Ser Gln Gln Gln Glu Gln Lys Gly Asp
 50 115 120 125
 52 Ala Pro Thr Cys Gly Ile Cys His Lys Thr Lys Phe Ala Asp Gly Cys
 53 130 135 140
 55 Gly His Asn Cys Ser Tyr Cys Gln Thr Lys Phe Cys Ala Arg Cys Gly
 56 145 150 155 160
 58 Gly Arg Val Ser Leu Arg Ser Asn Lys Val Met Trp Val Cys Asn Leu
 59 165 170 175
 61 Cys Arg Lys Gln Gln Glu Ile Leu Thr Lys Ser Gly Ala Trp Phe Tyr
 62 180 185 190
 64 Asn Ser Gly Ser Asn Thr Leu Gln Gln Pro Asp Gln Lys Val Pro Arg
 65 195 200 205
 67 Gly Leu Arg Asn Glu Glu Ala Pro Gln Glu Lys Lys Ala Lys Leu His
 68 210 215 220
 70 Glu Gln Pro Gln Phe Gln Gly Ala Pro Gly Asp Leu Ser Val Pro Ala
 71 225 230 235 240
 73 Val Glu Lys Gly Arg Ala His Gly Leu Thr Arg Gln Asp Thr Ile Lys

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74          245          250          255
76 Asn Gly Ser Gly Val Lys His Gln Ile Ala Ser Asp Met Pro Ser Asp
77          260          265          270
79 Arg Lys Arg Ser Pro Ser Val Ser Arg Asp Gln Asn Arg Arg Tyr Glu
80          275          280          285
82 Gln Ser Glu Glu Arg Glu Asp Tyr Ser Gln Tyr Val Pro Ser Asp Gly
83          290          295          300
85 Thr Met Pro Arg Ser Pro Ser Asp Tyr Ala Asp Arg Arg Ser Gln Arg
86 305          310          315          320
88 Glu Pro Gln Phe Tyr Glu Glu Pro Gly His Leu Asn Tyr Arg Asp Ser
89          325          330          335
91 Asn Arg Arg Gly His Arg His Ser Lys Glu Tyr Ile Val Asp Asp Glu
92          340          345          350
94 Asp Val Glu Ser Arg Asp Glu Tyr Glu Arg Gln Arg Arg Glu Glu Glu
95          355          360          365
97 Tyr Gln Ala Arg Tyr Arg Ser Asp Pro Asn Leu Ala Arg Tyr Pro Val
98          370          375          380
100 Lys Pro Gln Pro Tyr Glu Glu Gln Met Arg Ile His Ala Glu Val Ser
101 385          390          395          400
103 Arg Ala Arg His Glu Arg Arg His Ser Asp Val Ser Leu Ala Asn Ala
104          405          410          415
106 Glu Leu Glu Asp Ser Arg Ile Ser Leu Leu Arg Met Asp Arg Pro Ser
107          420          425          430
109 Arg Gln Arg Ser Val Ser Glu Arg Ala Ala Met Glu Asn Gln Arg
110          435          440          445
112 Ser Tyr Ser Met Glu Arg Thr Arg Glu Ala Gln Gly Gln Ser Ser Tyr
113          450          455          460
115 Pro Gln Arg Thr Ser Asn His Ser Pro Pro Thr Pro Arg Arg Ser Pro
116 465          470          475          480
118 Ile Pro Leu Asp Arg Pro Asp Met Arg Arg Ala Asp Ser Leu Arg Lys
119          485          490          495
121 Gln His His Leu Asp Pro Ser Ser Ala Val Arg Lys Thr Lys Arg Glu
122          500          505          510
124 Lys Met Glu Thr Met Leu Arg Asn Asp Ser Leu Ser Ser Asp Gln Ser
125          515          520          525
127 Glu Ser Val Arg Pro Pro Pro Pro Arg Pro His Lys Ser Lys Lys Gly
128          530          535          540
130 Gly Lys Met Arg Gln Val Ser Leu Ser Ser Ser Glu Glu Glu Leu Ala
131 545          550          555          560
133 Ser Thr Pro Glu Tyr Thr Ser Cys Asp Asp Val Glu Leu Glu Ser Glu
134          565          570          575
136 Ser Val Ser Glu Lys Gly Asp Ser Gln Lys Gly Lys Arg Lys Thr Ser
137          580          585          590
139 Glu Gln Gly Val Leu Ser Asp Ser Asn Thr Arg Ser Glu Arg Gln Lys
140          595          600          605
142 Lys Arg Met Tyr Tyr Gly Gly His Ser Leu Glu Glu Asp Leu Glu Trp
143          610          615          620
145 Ser Glu Pro Gln Ile Lys Asp Ser Gly Val Asp Thr Cys Ser Ser Thr
146 625          630          635          640

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148 Thr Leu Asn Glu Glu His Ser His Ser Asp Lys His Pro Val Thr Trp
149                               645                               650                               655
151 Gln Pro Ser Lys Asp Gly Asp Arg Leu Ile Gly Arg Ile Leu Leu Asn
152                               660                               665                               670
154 Lys Arg Leu Lys Asp Gly Ser Val Pro Arg Asp Ser Gly Ala Met Leu
155                               675                               680                               685
157 Gly Leu Lys Val Val Gly Gly Lys Met Thr Glu Ser Gly Arg Leu Cys
158                               690                               695                               700
160 Ala Phe Ile Thr Lys Val Lys Lys Gly Ser Leu Ala Asp Thr Val Gly
161 705                               710                               715                               720
163 His Leu Arg Pro Gly Asp Glu Val Leu Glu Trp Asn Gly Arg Leu Leu
164                               725                               730                               735
166 Gln Gly Ala Thr Phe Glu Glu Val Tyr Asn Ile Ile Leu Glu Ser Lys
167                               740                               745                               750
169 Pro Glu Pro Gln Val Glu Leu Val Val Ser Arg Pro Ile Gly Asp Ile
170                               755                               760                               765
172 Pro Arg Ile Pro Asp Ser Thr His Ala Gln Leu Glu Ser Ser Ser Ser
173                               770                               775                               780
175 Ser Phe Glu Ser Gln Lys Met Asp Arg Pro Ser Ile Ser Val Thr Ser
176 785                               790                               795                               800
178 Pro Met Ser Pro Gly Met Leu Arg Asp Val Pro Gln Phe Leu Ser Gly
179                               805                               810                               815
181 Gln Leu Ser Ile Lys Leu Trp Phe Asp Lys Val Gly His Gln Leu Ile
182                               820                               825                               830
184 Val Thr Ile Leu Gly Ala Lys Asp Leu Pro Ser Arg Glu Asp Gly Arg
185                               835                               840                               845
187 Pro Arg Asn Pro Tyr Val Lys Ile Tyr Phe Leu Pro Asp Arg Ser Asp
188                               850                               855                               860
190 Lys Asn Lys Arg Arg Thr Lys Thr Val Lys Lys Thr Leu Glu Pro Lys
191 865                               870                               875                               880
193 Trp Asn Gln Thr Phe Ile Tyr Ser Pro Val His Arg Arg Glu Phe Arg
194                               885                               890                               895
196 Glu Arg Met Leu Glu Ile Thr Leu Trp Asp Gln Ala Arg Val Arg Glu
197                               900                               905                               910
199 Glu Glu Ser Glu Phe Leu Gly Glu Ile Leu Ile Glu Leu Glu Thr Ala
200                               915                               920                               925
202 Leu Leu Asp Asp Glu Pro His Trp Tyr Lys Leu Gln Thr His Asp Val
203                               930                               935                               940
205 Ser Ser Leu Pro Leu Pro Arg Pro Ser Pro Tyr Leu Pro Arg Arg Gln
206 945                               950                               955                               960
208 Leu His Gly Glu Ser Pro Thr Arg Arg Leu Gln Arg Ser Lys Arg Ile
209                               965                               970                               975
211 Ser Asp Ser Glu Val Ser Asp Tyr Asp Cys Glu Asp Gly Val Gly Val
212                               980                               985                               990
214 Val Ser Asp Tyr Arg His Asn Gly Arg Asp Leu Gln Ser Ser Thr Leu
215                               995                               1000                               1005
217 Ser Val Pro Glu Gln Val Met Ser Ser Asn His Cys Ser Pro Ser
218 1010                               1015                               1020
220 Gly Ser Pro His Arg Val Asp Val Ile Gly Arg Thr Arg Ser Trp

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221	1025	1030	1035
223	Ser Pro Ser Ala Pro Pro Pro	Gln Arg Asn Val	Glu Gln Gly His
224	1040	1045	1050
226	Arg Gly Thr Arg Ala Thr Gly	His Tyr Asn Thr	Ile Ser Arg Met
227	1055	1060	1065
229	Asp Arg His Arg Val Met Asp	Asp His Tyr Ser	Ser Asp Arg Asp
230	1070	1075	1080
232	Arg Asp Cys Glu Ala Ala Asp	Arg Gln Pro Tyr	His Arg Ser Arg
233	1085	1090	1095
235	Ser Thr Glu Gln Arg Pro Leu	Leu Glu Arg Thr	Thr Thr Arg Ser
236	1100	1105	1110
238	Arg Ser Ser Glu Arg Pro Asp	Thr Asn Leu Met	Arg Ser Met Pro
239	1115	1120	1125
241	Ser Leu Met Thr Gly Arg Ser	Ala Pro Pro Ser	Pro Ala Leu Ser
242	1130	1135	1140
244	Arg Ser His Pro Arg Thr Gly	Ser Val Gln Thr	Ser Pro Ser Ser
245	1145	1150	1155
247	Thr Pro Gly Thr Gly Arg Arg	Gly Arg Gln Leu	Pro Gln Leu Pro
248	1160	1165	1170
250	Pro Lys Gly Thr Leu Glu Arg	Ser Ala Met Asp	Ile Glu Glu Arg
251	1175	1180	1185
253	Asn Arg Gln Met Lys Leu Asn	Lys Tyr Lys Gln	Val Ala Gly Ser
254	1190	1195	1200
256	Asp Pro Arg Leu Glu Gln Asp	Tyr His Ser Lys	Tyr Arg Ser Gly
257	1205	1210	1215
259	Trp Asp Pro His Arg Gly Ala	Asp Thr Val Ser	Thr Lys Ser Ser
260	1220	1225	1230
262	Asp Ser Asp Val Ser Asp Val	Ser Ala Val Ser	Arg Thr Ser Ser
263	1235	1240	1245
265	Ala Ser Arg Phe Ser Ser Thr	Ser Tyr Met Ser	Val Gln Ser Glu
266	1250	1255	1260
268	Arg Pro Arg Gly Asn Arg Lys	Ile Ser Val Phe	Thr Ser Lys Met
269	1265	1270	1275
271	Gln Asn Arg Gln Met Gly Val	Ser Gly Lys Asn	Leu Thr Lys Ser
272	1280	1285	1290
274	Thr Ser Ile Ser Gly Asp Met	Cys Ser Leu Glu	Lys Asn Asp Gly
275	1295	1300	1305
277	Ser Gln Ser Asp Thr Ala Val	Gly Ala Leu Gly	Thr Ser Gly Lys
278	1310	1315	1320
280	Lys Arg Arg Ser Ser Ile Gly	Ala Lys Met Val	Ala Ile Val Gly
281	1325	1330	1335
283	Leu Ser Arg Lys Ser Arg Ser	Ala Ser Gln Leu	Ser Gln Thr Glu
284	1340	1345	1350
286	Gly Gly Gly Lys Lys Leu Arg	Ser Thr Val Gln	Arg Ser Thr Glu
287	1355	1360	1365
289	Thr Gly Leu Ala Val Glu Met	Arg Asn Trp Met	Thr Arg Gln Ala
290	1370	1375	1380
292	Ser Arg Glu Ser Thr Asp Gly	Ser Met Asn Ser	Tyr Ser Ser Glu
293	1385	1390	1395

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295 Gly Asn Leu Ile Phe Pro Gly Val Arg Leu Ala Ser Asp Ser Gln
296      1400      1405      1410
298 Phe Ser Asp Phe Leu Asp Gly Leu Gly Pro Ala Gln Leu Val Gly
299      1415      1420      1425
301 Arg Gln Thr Leu Ala Thr Pro Ala Met Gly Asp Ile Gln Val Gly
302      1430      1435      1440
304 Met Met Asp Lys Lys Gly Gln Leu Glu Val Glu Ile Ile Arg Ala
305      1445      1450      1455
307 Arg Gly Leu Val Val Lys Pro Gly Ser Lys Thr Leu Pro Ala Pro
308      1460      1465      1470
310 Tyr Val Lys Val Tyr Leu Leu Asp Asn Gly Val Cys Ile Ala Lys
311      1475      1480      1485
313 Lys Lys Thr Lys Val Ala Arg Lys Thr Leu Glu Pro Leu Tyr Gln
314      1490      1495      1500
316 Gln Leu Leu Ser Phe Glu Glu Ser Pro Gln Gly Arg Val Leu Gln
317      1505      1510      1515
319 Ile Ile Val Trp Gly Asp Tyr Gly Arg Met Asp His Lys Ser Phe
320      1520      1525      1530
322 Met Gly Val Ala Gln Ile Leu Leu Asp Glu Leu Glu Leu Ser Asn
323      1535      1540      1545
325 Met Val Ile Gly Trp Phe Lys Leu Phe Pro Pro Ser Ser Leu Val
326      1550      1555      1560
328 Asp Pro Thr Ser Ala Pro Leu Thr Arg Arg Ala Ser Gln Ser Ser
329      1565      1570      1575
331 Leu Glu Ser Ser Thr Gly Pro Ser Tyr Ser Arg Ser
332      1580      1585      1590

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334 <210> SEQ ID NO: 2

335 <211> LENGTH: 4980

336 <212> TYPE: DNA

337 <213> ORGANISM: Mus musculus

339 <400> SEQUENCE: 2

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344 ccacctcagc gaagaggaga ggaaaatcat cctggctgtc atggatcgtc agaagaaaga      180
346 agaggagaag gagcagtcgc tgctcaagat caaagaagaa cacaaagcac aaccgacaca      240
348 gtggtttccc tttagtggga tcaactgaact ggtaaataac gttctgcagc cccagcaaaa      300
350 acaacccaat gagaaggagc cccagacaaa gctgcaccaa caatttgaaa tgtataagga      360
352 gcaagtcaag aagatgggag aggaatcgca gcagcagcaa gagcagaagg gtgatgcccc      420
354 gacctgtggc atctgccaca agacaaaatt tgcagatgga tgcggccata attgttcta      480
356 ttgccaaacc aagttctgtg ctogatgtgg aggtcagatg tctttacgct caaacaaggt      540
358 tatgtgggtg tgtaatttgt gcgaaaaca acaagaaatc ctactaaat caggagcatg      600
360 gttttataat agtgggtcta acacactgca gcaacctgat caaaagggtc ctcgagggct      660
362 tcgaaatgag gaagcccctc aggagaagaa agcaaaacta cacgagcagc cccagttcca      720
364 aggagcccca ggtgacttat cagtacctgc agttgagaaa ggccgagctc atgggctcac      780
366 aagacaggat actattaaaa atggatcagg agtgaagcac cagattgcca gtgacatgcc      840
368 ttcagacaga aaacgaagtc catcagtgtc cagggatcaa aatcgaagat acgagcaaag      900
370 tgaagaaaga gaggactact cacagtatgt tccttcagat ggtacaatgc caagatctcc      960
372 ttcggattat gctgatagac gatctcagcg tgagcctcaa ttttatgaag aacctggtca      1020
374 tttaaattac agggattcta acaggagagg ccatagacat tccaaagagt atattgtgga      1080

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